

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/763,748

DATE: 08/03/2001

TIME: 14:04:36

Input Set : A:\Pto.amc

Output Set: N:\CRF3\08032001\I763748.raw

```

3 <110> APPLICANT: Brett P. Monia and Lex M. Cowsert
5 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
7 <130> FILE REFERENCE: RTSP-0100
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/763,748
C--> 10 <141> CURRENT FILING DATE: 2001-02-27
12 <150> PRIOR APPLICATION NUMBER: 09/143,212
13 <151> PRIOR FILING DATE: 1998-08-28
15 <160> NUMBER OF SEQ ID NOS: 87
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1435
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)..(987)
26 <400> SEQUENCE: 1
27   ctg gcg ggc gtg gga acc cag gcc ccg ccg agg cgg cca gga ggt gag      48
28   Leu Ala Gly Val Gly Thr Gln Ala Pro Pro Arg Arg Pro Gly Gly Glu
29     1          5          10          15
31   atg gca gct ggg caa aat ggg cac gaa gag tgg gtg ggc agc gca tac      96
32   Met Ala Ala Gly Gln Asn Gly His Glu Glu Trp Val Gly Ser Ala Tyr
33     20          25          30
35   ctg ttt gtg gag tcc tcg ctg gac aag gtg gtc ctg tcg gat gcc tac      144
36   Leu Phe Val Glu Ser Ser Leu Asp Lys Val Val Leu Ser Asp Ala Tyr
37     35          40          45
39   gcg cac ccc cag cag aag gtg gca gtg tac agg gct ctg cag gct gcc      192
40   Ala His Pro Gln Gln Lys Val Ala Val Tyr Arg Ala Leu Gln Ala Ala
41     50          55          60
43   ttg gca gag agc ggc ggg agc ccg gac gtg ctg cag atg ctg aag atc      240
44   Leu Ala Glu Ser Gly Gly Ser Pro Asp Val Leu Gln Met Leu Lys Ile
45     65          70          75          80
47   cac cgc agc gac ccg cag ctg atc gtg cag ctg cga ttc tgc ggg cgg      288
48   His Arg Ser Asp Pro Gln Leu Ile Val Gln Leu Arg Phe Cys Gly Arg
49     85          90          95
51   cag ccc tgt ggc cgc ttc ctc cgc gcc tac cgc gag ggg gcg ctg cgc      336
52   Gln Pro Cys Gly Arg Phe Leu Arg Ala Tyr Arg Glu Gly Ala Leu Arg
53    100         105         110
55   gcc gcg ctg cag agg agc ctg gcg gcc gcg ctc gcc cag cac tcg gtg      384
56   Ala Ala Leu Gln Arg Ser Leu Ala Ala Ala Leu Ala Gln His Ser Val
57    115         120         125
59   ccg ctg caa ctg gag ctg cgc gcc ggc gcc gag cgg ctg gac gct ttg      432
60   Pro Leu Gln Leu Glu Leu Arg Ala Gly Ala Glu Arg Leu Asp Ala Leu
61    130         135         140
63   ctg gcg gac gag gag cgc tgt ttg agt tgc atc cta gcc cag cag ccc      480
64   Leu Ala Asp Glu Glu Arg Cys Leu Ser Cys Ile Leu Ala Gln Gln Pro
65    145         150         155         160
67   gac cgg ctc cgg gat gaa gaa ctg gct gag ctg gag gat gcg ctg cga      528

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68  Asp Arg Leu Arg Asp Glu Glu Leu Ala Glu Leu Glu Asp Ala Leu Arg
69          165                      170                      175
71  aat ctg aag tgc ggc tcg ggg gcc cgg ggt ggc gac ggg gag gtc gct      576
72  Asn Leu Lys Cys Gly Ser Gly Ala Arg Gly Gly Asp Gly Glu Val Ala
73          180                      185                      190
75  tcg gcc ccc ttg cag ccc ccg gtg ccc tct ctg tcg gag gtg aag ccg      624
76  Ser Ala Pro Leu Gln Pro Pro Val Pro Ser Leu Ser Glu Val Lys Pro
77          195                      200                      205
79  ccg ccg ccg ccg cca cct gcc cag act ttt ctg ttc cag ggt cag cct      672
80  Pro Pro Pro Pro Pro Pro Ala Gln Thr Phe Leu Phe Gln Gly Gln Pro
81          210                      215                      220
83  gta gtg aat cgg ccg ctg agc ctg aag gac caa cag acg ttc gcg cgc      720
84  Val Val Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg
85          225                      230                      235                      240
87  tct gtg ggt ctc aaa tgg cgc aag gtg ggg cgc tca ctg cag cga ggc      768
88  Ser Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly
89          245                      250                      255
91  tgc cgg gcg ctg cgg gac ccg gcg ctg gac tcg ctg gcc tac gag tac      816
92  Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu Tyr
93          260                      265                      270
95  gag cgc gag gga ctg tac gag cag gcc ttc cag ctg ctg cgg cgc ttc      864
96  Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg Arg Phe
97          275                      280                      285
99  gtg cag gcc gag ggc cgc cgc gcc acg ctg cag cgc ctg gtg gag gca      912
100 Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu Val Glu Ala
101          290                      295                      300
103  ctc gag gag aac gag ctc acc agc ctg gca gag gac ttg ctg ggc ctg      960
104  Leu Glu Glu Asn Glu Leu Thr Ser Leu Ala Glu Asp Leu Leu Gly Leu
105          305                      310                      315                      320
107  acc gat ccc aat ggc ggc ctg gcc tag accaggggtg cagccagctt      1007
108  Thr Asp Pro Asn Gly Gly Leu Ala
109          325
111  ttggagaacc tggatggcct tagggttcct tctgcggcta ttgctgaacc cctgtccatc 1067
113  cacgggaccc tgaaactcca cttggcctat ctgctggacc tgctggggca gagttgattg 1127
115  ccttccccag gagccagacc actgggggtg catcattggg gattctgcct caggtacttt 1187
117  gatagagtgt ggggtggggg ggacttgctt tggagatcag cctcaccttc tcccatccca 1247
119  gaagcggggc ttacagccag cccttacagt ttcactcatg aagcaccttg atctttggtg 1307
121  tcctggactt catcctgggt gctgcagata ctgcagtga gtaaaacagg aatcaatctt 1367
123  gcctgcccc agctcacact cagcgtggga ccccgaatgt taagcaatga taataaagta 1427
125  taacacgg                                     1435
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 20
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Synthetic
136 <400> SEQUENCE: 2
137  acgaggagcg ctgtttgagt                                     20
140 <210> SEQ ID NO: 3

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141 <211> LENGTH: 22
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Synthetic
148 <400> SEQUENCE: 3
149     tccagctcag ccagttcttc at                                22
152 <210> SEQ ID NO: 4
153 <211> LENGTH: 19
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Synthetic
160 <400> SEQUENCE: 4
161     ccagcagccc gaccggctc                                19
164 <210> SEQ ID NO: 5
165 <211> LENGTH: 19
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: Synthetic
172 <400> SEQUENCE: 5
173     gaagggtgaag gtcggagtc                                19
176 <210> SEQ ID NO: 6
177 <211> LENGTH: 20
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Synthetic
184 <400> SEQUENCE: 6
185     gaagatggtg atgggatttc                                20
188 <210> SEQ ID NO: 7
189 <211> LENGTH: 20
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Synthetic
196 <400> SEQUENCE: 7
197     caagcttccc gttctcagcc                                20
200 <210> SEQ ID NO: 8
201 <211> LENGTH: 18
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Synthetic
W--> 207 <400> SEQUENCE: 8
208     ggttcccacg cccgccag                                18
211 <210> SEQ ID NO: 9
212 <211> LENGTH: 18

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213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Synthetic
219 <400> SEQUENCE: 9
220     ctcacctcct ggccgcct                                18
223 <210> SEQ ID NO: 10
224 <211> LENGTH: 18
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Synthetic
231 <400> SEQUENCE: 10
232     agctgccatc tcacctcc                                18
235 <210> SEQ ID NO: 11
236 <211> LENGTH: 18
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Synthetic
243 <400> SEQUENCE: 11
244     ctcttcgtgc ccattttg                                18
247 <210> SEQ ID NO: 12
248 <211> LENGTH: 18
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Synthetic
255 <400> SEQUENCE: 12
256     caccactct tcgtgccc                                18
259 <210> SEQ ID NO: 13
260 <211> LENGTH: 18
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Synthetic
267 <400> SEQUENCE: 13
268     gctgccacc cactcttc                                18
271 <210> SEQ ID NO: 14
272 <211> LENGTH: 18
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Synthetic
279 <400> SEQUENCE: 14
280     ggtatgcgct gccacccc                                18
283 <210> SEQ ID NO: 15
284 <211> LENGTH: 18
285 <212> TYPE: DNA

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286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Synthetic
291 <400> SEQUENCE: 15
292     tccacaaaca ggtatgcg                                18
295 <210> SEQ ID NO: 16
296 <211> LENGTH: 18
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Synthetic
303 <400> SEQUENCE: 16
304     gaggactcca caaacagg                                18
307 <210> SEQ ID NO: 17
308 <211> LENGTH: 18
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Synthetic
315 <400> SEQUENCE: 17
316     gtccagcgag gactccac                                18
319 <210> SEQ ID NO: 18
320 <211> LENGTH: 18
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Synthetic
327 <400> SEQUENCE: 18
328     ccaccttgtc cagcgagg                                18
331 <210> SEQ ID NO: 19
332 <211> LENGTH: 18
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Synthetic
339 <400> SEQUENCE: 19
340     gcatccgaca ggaccacc                                18
343 <210> SEQ ID NO: 20
344 <211> LENGTH: 18
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Synthetic
351 <400> SEQUENCE: 20
352     gcgtaggcat ccgacagg                                18
355 <210> SEQ ID NO: 21
356 <211> LENGTH: 18
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:207 M:283 W: Missing Blank Line separator, <400> field identifier